SEQUENCE LISTING

<110> Kimoto, Norihiro
Yamamoto, Hircaki
Mitsuhashi, Kazuya

<120> NOVEL CARBONYL REDUCTASE, METHOD FOR PRODUCING SAID ENZYME, DNA ENCODING SAID ENZYME, AND METHOD FOR PRODUCING ALCOHOL USING SAID ENZYME

<130> 06501-050001

<140> US 09/468,738
<141> 1999-12-21

<150> JP 1999-171160
<151> 1999-06-17

<150> JP 1998-363130
<151> 1998-12-21

<160> 29

<170> PatentIn Ver. 2.0, reformatted using WordPerfect 5.1

<210> 1
<211> 879
<212> DNA
<213> Kluyveromyces aestuarii

<400> 1
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ttgacagtta tcactggtgg agcaggagcc attggcggag ctctgtgtga gggatttgcg 180
tcctgtggat ctgacgttgt cattttagat tacaaataca gtcctgaatt gtcatcagtt 240
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gacgtgaaac ttgttgttgc aaagatttta gaagattttc ctgatcgcga tatcaataca 360
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ccagatgtgt ggaaacgtgt tatggatgtg aacgtgcaag gaacttatca ttgtgcgaaa 480
tatgtggcag aagtgttcaa acaacagggc catggtaatc tgattttgac tgcgtcgatg 540
tcaagttata taagcaacgt tcccaactac caaacatgtt ataatgcctc taaagcggcc 600
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aaaatcagat gcaattcggt ttcacctggt tacactgaca ccgcactttc agcttttgtt 720
ccggtcgaac agcgcgctca gtggtgggga ttgactccta tgggtcgcga agcattacca 780
caagagctag tcggagccta cttgtatttg gcatctgacg ctgcatcatt cacaaatgga 840
tgtgatattc aagtagacgg tgggtacact tgcgtttga 879

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<211> 292
<212> PRT
<213> Kluyveromyces aestuarii

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Pro Gln Glu Pro Pro Lys Glu Gln Tyr Pro Asp Gly Val Asn Tyr Leu

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Ser Leu Phe Ser Gln Lys Gly Lys Leu Thr Val Ile Thr Gly Gly Ala
        35                  40                  45
Gly Ala Ile Gly Gly Ala Leu Cys Glu Gly Phe Ala Ser Cys Gly Ser
    50                  55                  60
Asp Val Val Ile Leu Asp Tyr Lys Tyr Ser Pro Glu Leu Ser Ser Val
65                  70                  75                  80
Leu Glu Ser Arg Tyr Gly Val Arg Ser Lys Ser Tyr Gln Val Asp Ile
                85                  90                  95
Thr Ser Ser Glu Asp Val Lys Leu Val Val Ala Lys Ile Leu Glu Asp
            100                 105                 110
Phe Pro Asp Arg Asp Ile Asn Thr Phe Val Ala Asn Ala Gly Ile Ala
        115                 120                 125
Trp Thr Asn Gly Ser Ile Leu Asn Glu Asn Ala Thr Pro Asp Val Trp
    130                 135                 140
Lys Arg Val Met Asp Val Asn Val Gln Gly Thr Tyr His Cys Ala Lys
145                 150                 155                 160
Tyr Val Ala Glu Val Phe Lys Gln Gln Gly His Gly Asn Leu Ile Leu
                165                 170                 175
Thr Ala Ser Met Ser Ser Tyr Ile Ser Asn Val Pro Asn Tyr Gln Thr
            180                 185                 190
Cys Tyr Asn Ala Ser Lys Ala Ala Val Arg His Met Ala Lys Gly Phe
        195                 200                 205
Ala Val Glu Phe Ala His Leu Thr Asn Pro Ala Gly Lys Ile Arg Cys
    210                 215                 220
Asn Ser Val Ser Pro Gly Tyr Thr Asp Thr Ala Leu Ser Ala Phe Val
225                 230                 235                 240
Pro Val Glu Gln Arg Ala Gln Trp Trp Gly Leu Thr Pro Met Gly Arg
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Glu Ala Leu Pro Gln Glu Leu Val Gly Ala Tyr Leu Tyr Leu Ala Ser
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Asp Ala Ala Ser Phe Thr Asn Gly Cys Asp Ile Gln Val Asp Gly Gly
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<213> Kluyveromyces aestuarii

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<210> 4
<211> 10
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<213> Kluyveromyces aestuarii

<400> 4
Tyr Ser Pro Glu Leu Ser Ser Val Leu Glu
1 5 10

<210> 5
<211> 10
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<213> Kluyveromyces aestuarii

<400> 5
Gly Phe Ala Val Glu Phe Ala His Leu Thr
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<210> 6
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized Primer Sequence

<400> 6
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 7
gtgaagcttc cwccyctyar raartgytgr aawgt 35

<210> 8
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized Primer Sequence

<400> 8
gacggatcct aytstccwga rttrtsttst gtwttrga 38

<210> 9
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized Primer Sequence

<400> 9
gtgaagcttt cyaawacasa asayaaytcw ggasarta 38

<210> 10
<211> 32
<212> DNA
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<220>
<223> Artificially Synthesized Primer Sequence

<221> misc_feature
<222> (0)...(0)
<223> n = A, T, G, or C

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<212> DNA
<213> Kluyveromyces aestuarii

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aaattgacag ttatcactgg tggagcagga gccattggcg gagctctgtg tgagggattt 180
gcgtcctgtg gatctgacgt tgtcatttta gattacaaat actctcctga attatcttct 240
gtattagaaa gctt 254

<210> 13
<211> 650
<212> DNA
<213> Kluyveromyces aestuarii

<400> 13
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ccaccgaagg agcaatatcc cgatggtgtt aattacttga gcttgttcag tcagaaaggg 120
aaattgacag ttatcactgg tggagcagga gccattggcg gagctctgtg tgagggattt 180
gcgtcctgtg gatctgacgt tgtcatttta gattacaaat acagtcctga attgtcatca 240
gttttggaat ctaggtatgg agtgaggtcg aaaagctatc aggtcgacat tacgagttca 300
gaagacgtga aacttgttgt tgcaaagatt ttagaagatt ttcctgatcg cgatatcaat 360
acatttgttg ctaatgcagg tattgcatgg accaacggtt ccattttgaa cgaaaacgcg 420
acgccagatg tgtggaaacg tgttatggat gtgaacgtgc aaggaactta tcattgtgcg 480
aaatatgtgg cagaagtgtt caaacaacag ggccatggta atctgatttt gactgcgtcg 540
atgtcaagtt atataagcaa cgttcccaac taccaaacat gttataatgc ctctaaagcg 600
gccgtcagac atatggcaaa gggttttgca gtagagttcg cacaaagctt 650

<210> 14
<211> 437
<212> DNA
<213> Kluyveromyces aestuarii

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gaagattttc ctgatcgcga tatcaataca tttgttgcta atgcaggtat tgcatggacc 180
aacggttcca ttttgaacga aaacgcgacg ccagatgtgt ggaaacgtgt tatggatgtg 240
aacgtgcaag gaacttatca ttgtgcgaaa tatgtggcag aagtgttcaa acaacagggc 300
catggtaatc tgattttgac tgcgtcgatg tcaagttata taagcaacgt tcccaactac 360
caaacatgtt ataatgcctc taaagcggcc gtcagacata tggcaaaggg attcgcagta 420
gaattcgctc aaagctt 437

<210> 15
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized Primer Sequence

<400> 15
tcggtggctc ctgaggaac 19

<210> 16
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized Primer Sequence

<400> 16
acatgttata atgcctctaa agc 23

<210> 17
<211> 1787
<212> DNA
<213> Kluyveromyces aestuarii

<221> misc_feature
<222> (0)...(0)
<223> n = A, T, G, or C

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maagacaagg cgraatagat gacgracgtt ggctgtaaat gtcgggggac naaatagatg 180
caaatawtws wgmnaymwww gkmmymkwyn ttttttaaat agcctggtta actacggcag 240
catgggctcg gtggtaggga aagaacaatt agtctatatt taggagagag gtataaataa 300
atgaaaagat gcatatggaa attggataat ttcacacaat ttacgatgga ctgatctgta 360
catgaactct ttgatatgta tcttatgtta tttttccttt aagcgacttc atagtggttt 420
cgggcctcgt tcatcggaga gctagctttg cacctgagtt tgggtttaga cacactataa 480
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ccccanagtt gcyyymymyc ycaaraatga cmttgttaaw mmsywtgtwr aaacacggca 1560
gttyccyatg gtattgattc gatgagttac aactttcatc acgtaaaaat gccagaaaaa 1620
aaaaggttgt taatcaaata gacacgcttt cgaaaccatg catcaaacgg tcctaaacag 1680
aacaatacag gacactgtgc agcatggtat cggcaatcca aagcttcata tccacaagac 1740
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<210> 18
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized Primer Sequence

<400> 18
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<210> 19
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized Primer Sequence

<400> 19
tgttctagat taaacgcaag tgtacccacc g 31

<210> 20
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized Primer Sequence

<400> 20
tctgtatcag gctgaaaatc ttc 23

<210> 21
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized Primer Sequence

<400> 21
atatattaat gtatcgatta aataaggag 29

<210> 22
<211> 891
<212> DNA
<213> Kluyveromyces aestuarii

<400> 22
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cagaaaggga aattgacagt tatcactggt ggagcaggag ccattggcgg agctctgtgt 180
gagggatttg cgtcctgtgg atctgacgtt gtcattttag attacaaata cagtcctgaa 240
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actgcgtcga tgtcaagtta tataagcaac gttcccaact accaaacatg ttataatgcc 600
tctaaagcgg ccgtcagaca tatggcaaag ggatttgctg ttgaattcgc ccatttgaca 660
aaccccgcag gtaaaatcag atgcaattcg gtttcacctg gttacactga caccgcactt 720
tcagcttttg ttccggtcga acagcgcgct cagtggtggg gattgactcc tatgggtcgc 780
gaagcattac cacaagagct agtcggagcc tacttgtatt tggcatctga cgctgcatca 840
ttcacaaatg gatgtgatat tcaagtagac ggtgggtaca cttgcgttta a 891

<210> 23
<211> 296
<212> PRT
<213> Kluyveromyces aestuarii

<400> 23
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20 25 30
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35 40 45
Thr Gly Gly Ala Gly Ala Ile Gly Gly Ala Leu Cys Glu Gly Phe Ala
50 55 60
Ser Cys Gly Ser Asp Val Val Ile Leu Asp Tyr Lys Tyr Ser Pro Glu
65 70 75 80
Leu Ser Ser Val Leu Glu Ser Arg Tyr Gly Val Arg Ser Lys Ser Tyr
85 90 95
Gln Val Asp Ile Thr Ser Ser Glu Asp Val Lys Leu Val Val Ala Lys
100 105 110
Ile Leu Glu Asp Phe Pro Asp Arg Asp Ile Asn Thr Phe Val Ala Asn
115 120 125
Ala Gly Ile Ala Trp Thr Asn Gly Ser Ile Leu Asn Glu Asn Ala Thr
130 135 140
Pro Asp Val Trp Lys Arg Val Met Asp Val Asn Val Gln Gly Thr Tyr
145 150 155 160
His Cys Ala Lys Tyr Val Ala Glu Val Phe Lys Gln Gln Gly His Gly
165 170 175
Asn Leu Ile Leu Thr Ala Ser Met Ser Ser Tyr Ile Ser Asn Val Pro
180 185 190
Asn Tyr Gln Thr Cys Tyr Asn Ala Ser Lys Ala Ala Val Arg His Met

195 200 205
Ala Lys Gly Phe Ala Val Glu Phe Ala His Leu Thr Asn Pro Ala Gly
210 215 220
Lys Ile Arg Cys Asn Ser Val Ser Pro Gly Tyr Thr Asp Thr Ala Leu
225 230 235 240
Ser Ala Phe Val Pro Val Glu Gln Arg Ala Gln Trp Trp Gly Leu Thr
245 250 255
Pro Met Gly Arg Glu Ala Leu Pro Gln Glu Leu Val Gly Ala Tyr Leu
260 265 270
Tyr Leu Ala Ser Asp Ala Ala Ser Phe Thr Asn Gly Cys Asp Ile Gln
275 280 285
Val Asp Gly Gly Tyr Thr Cys Val
290 295

<210> 24
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized Primer Sequence

<400> 24
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<210> 25
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized Primer Sequence

<400> 25
ctagttttag aattcctcta gattactcga g 31

<210> 26
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized Primer Sequence

<400> 26
gaggaattca tacatgtatc cagatttaaa aggaa 35

<210> 27
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized Primer Sequence

<400> 27
ggtaagcttt cattaaccgc ggcctgcctg 30

<210> 28
<211> 786
<212> DNA
<213> Bacillus subtilis

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aaggcgatgg ccattcgctt cggcaaggag caggcaaaag tggttatcaa ctattatagt 120
aataaacaag atccgaacga ggtaaaagaa gaggtcatca aggcgggcgg tgaagctgtt 180
gtcgtccaag gagatgtcac gaaagaggaa gatgtaaaaa atatcgtgca aacggcaatt 240
aaggagttcg gcacactcga tattatgatt aataatgccg gtcttgaaaa tcctgtgcca 300
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attaacatgt ccagtgtgca cgaagtgatt ccttggccgt tatttgtcca ctatgcggca 480
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attcgcgtca ataatattgg gccaggtgcg atcaacacgc caatcaatgc tgaaaaattc 600
gctgacccta aacagaaagc tgatgtagaa agcatgattc caatgggata tatcggcgaa 660
ccggaggaga tcgccgcagt agcagcctgg cttgcttcga aggaagccag ctacgtcaca 720
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ggttaa 786

<210> 29
<211> 261
<212> PRT
<213> Bacillus subtilis

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Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
20 25 30
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
35 40 45
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
50 55 60
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
65 70 75 80
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
85 90 95
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
100 105 110
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
115 120 125
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
130 135 140
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145 150 155 160
Ser Lys Gly Gly Ile Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
165 170 175
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
180 185 190
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp
195 200 205
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
210 215 220
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr

225 230 235 240
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
245 250 255
Gln Ala Gly Arg Gly
260